

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

ROBERTSON, Daniel E.

MURPHY, Dennis

REID, John

MAFFIA, Anthony

LINK, Steven

SWANSON, Ronald V.

WARREN, Patrick V.

KOSMOTKA, Anna

(ii) TITLE OF INVENTION:

ESTERASES

(iii) NUMBER OF SEQUENCES: 42

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN

(B) STREET: 6 BECKER FARM ROAD

(C) CITY: ROSELAND

(D) STATE: NEW JERSEY

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 INCH DISKETTE

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: WORD PERFECT 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unassigned

(B) FILING DATE: Concurrently

(C) CLASSIFICATION: Unassigned

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HERRON, CHARLES J.

(B) REGISTRATION NUMBER: 28,019

(C) REFERENCE/DOCKET NUMBER: 331400-39

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700

(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGTCTTTA AACAGCACT CT

52

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGATCT CTATCGTTTA GTGTATGATT T

31

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAACTC CTTGAGCCCA CA

52

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGATCT CGCCGGTACA CCATCAGCCA C

31

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGCCATAT GTTAGGAATG GT

52

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 53 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAGGTACC TTAGAACTGT GCTGAAGAAA TAAATTCGTC CATTGCTCTA TTA

53

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 49 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGAGGTACC TTAGAACTGT GCTGAAGAAA TAAATTCGTC CATTGCTCT

49

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 53 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAGATTG AGGAAATTTG AAG

53

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGAGGTACC CTATTCAGAA AGTACCTCTA A

31

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGTTTAAT ATCAATGTCT TT

52

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGGAAGATCT TTAAGGATTT TCCCTGGGTA G

31

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGGAGGTT TACAAGGCCA AA

52

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGAGGTACC TTATTGAGCC GAAGAGTACG A

31

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 53 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGATTGGC AATTGAAAT TGA

53

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGAGGTACC TTAAAGTGCT CTCATATCCC C

31

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGCCAGCT AATGACTCAC CC

52

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 32 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
CGGAAGATCT TCAACAGGCT CCAAATAATT TC 32

(2) INFORMATION FOR SEQ ID NO:18:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 29 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAAGATCT ACAGGCTCCA AATAATTTC 29

(2) INFORMATION FOR SEQ ID NO:19:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGCTTGAT ATGCCAATCG AC 52

(2) INFORMATION FOR SEQ ID NO:20:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGAGGTACC CTAGTCGAAC AGAAGAAGAG C 31

(2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGCCCTA GATCCTAGAA TT 52

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGGAGGTACC TTAAATTTTA TCATAAAATA C

31

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 555 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG TCT TTA AAC AAG CAC TCT TGG ATG GAT ATG ATA ATA TTT ATT CTC	48
Met Ser Leu Asn Lys His Ser Trp Met Asp Met Ile Ile Phe Ile Leu	
1 5 10 15	
AGC TTT TCT TTC CCA TTA ACA ATG ATC GCA TTA GCT ATC TCT ATG TCG	96
Ser Phe Ser Phe Pro Leu Thr Met Ile Ala Leu Ala Ile Ser Met Ser	
20 25 30	
TCA TGG TTT AAT ATA TGG AAT AAT GCA TTA AGC GAT CTA GGA CAT GCT	144
Ser Trp Phe Asn Ile Trp Asn Asn Ala Leu Ser Asp Leu Gly His Ala	
35 40 45	
GTT AAA AGC AGT GTT GCT CCA ATA TTC AAT CTA GGT CTT GCA ATT GGT	192
Val Lys Ser Ser Val Ala Pro Ile Phe Asn Leu Gly Leu Ala Ile Gly	
50 55 60	
GGG ATA CTA ATT GTT ATA GTT GGT TTA AGA AAT CTT TAT TCG TGG AGT	240
Gly Ile Leu Ile Val Ile Val Gly Leu Arg Asn Leu Tyr Ser Trp Ser	
65 70 75 80	
AGA GTT AAA GGA TCT TTA ATC ATA TCC ATG GGT GTA TTT CTT AAC TTA	288
Arg Val Lys Gly Ser Leu Ile Ile Ser Met Gly Val Phe Leu Asn Leu	
85 90 95	
ATA GGG GTT TTC GAC GAA GTA TAT GGT TGG ATA CAT TTC CTA GTC TCA	336
Ile Gly Val Phe Asp Glu Val Tyr Gly Trp Ile His Phe Leu Val Ser	
100 105 110	
GTA TTG TTT TTC TTA TCA ATA ATA GCA TAT TTC ATA GCT ATA TCA ATA	384
Val Leu Phe Phe Leu Ser Ile Ile Ala Tyr Phe Ile Ala Ile Ser Ile	
115 120 125	
CTT GAC AAA TCA TGG ATA GCT GTT CTA CTA ATA ATA GGT CAT ATT GCA	432
Leu Asp Lys Ser Trp Ile Ala Val Leu Leu Ile Ile Gly His Ile Ala	
130 135 140	
ATG TGG TAT CTA CAC TTT GCT TCA GAG ATT CCG AGA GGT GCT GCT ATT	480

Met Trp Tyr Leu His Phe Ala Ser Glu Ile Pro Arg Gly Ala Ala Ile
145 150 155 160

CCC GAG TTA TTA GCG GTA TTC TCG TTT TTA CCA TTC TAT ATA AGA CAG
Pro Glu Leu Leu Ala Val Phe Ser Phe Leu Pro Phe Tyr Ile Arg Asp
165 170 175

528

TAT TTT AAA TCA TAC ACT AAA CGA TAG
Tyr Phe Lys Ser Tyr Thr Lys Arg
180

576

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1041 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG AAA CTC CTT GAG CCC ACA AAT ACC TCC TAC ACG CTG TTA CAG GAT
Met Lys Leu Leu Glu Pro Thr Asn Thr Ser Tyr Thr Leu Leu Gln Asp
1 5 10 15

48

TTA GCA TTG CAT TTT GCA TTT TAC TGG TTT CTG GCC GTG TAT ACG TGG
Leu Ala Leu His Phe Ala Phe Tyr Trp Phe Leu Ala Val Tyr Thr Trp
20 25 30

96

TTA CCC GGT GTC CTA GTC CGG GGC GTA GCT GTG GAC ACA GGG GTG GCT
Leu Pro Gly Val Leu Val Arg Gly Val Ala Val Asp Thr Gly Val Ala
35 40 45

144

CGG GTG CCT GGG CTC GGC CGG CGC GGT AAG AGG CTG CTC CTG GCC GCT
Arg Val Pro Gly Leu Gly Arg Arg Gly Lys Arg Leu Leu Ala Ala
50 55 60

192

GTG GCT GTC TTG GCG CTT GTT GTG TCC GTT GTT GTC CCG GCT TAT GTG
Val Ala Val Leu Ala Leu Val Val Ser Val Val Val Pro Ala Tyr Val
65 70 75 80

240

GCG TAT AGT AGT CTG CAC CCG GAG AGC TGT CGG CCC GTT GCG CCG GAG
Ala Tyr Ser Ser Leu His Pro Glu Ser Cys Arg Pro Val Ala Pro Glu
85 90 95

288

GGG CTC ACC TAC AAA GAG TTC AGC GTG ACC GCG GAG GAT GGC TTG GTG
Gly Leu Thr Tyr Lys Glu Phe Ser Val Thr Ala Glu Asp Gly Leu Val
100 105 110

336

GTT CGG GGC TGG GTG CTG GGC CCC GGC GCT GGG GGC AAC CCG GTG TTC
Val Arg Gly Trp Cal Leu Gly Pro Gly Ala Gly Gly Asn Pro Val Phe
115 120 125

384

GTT TTG ATG CAC GGG TAT ACT GGG TGC CGC TCG GCG CCC TAC ATG GCT
Val Leu Met His Gly Tyr Thr Gly Cys Arg Ser Ala Pro Tyr Met Ala
130 135 140

432

GTG CTG GCC CGG GAG CTC GTG GAG TGG GGG TAC CCG GTG GTT GTG TTC
Val Leu Ala Arg Glu Leu Val Glu Trp Gly Tyr Pro Val Val Val Phe
145 150 155 160

480

GAC TTC CGG GGC CAC GGG GAG AGC GGG GGC TCG ACG ACG ATT GGG CCC Asp Phe Arg Gly His Gly Glu Ser Gly Gly Ser Thr Thr Ile Gly Pro 165 170 175	528
CGG GAG GTG CTG GAT GCC CGG GCT GTG GTG GGC TAT GTC TCG GAG CGG Arg Glu Val Leu Asp Ala Arg Ala Val Val Gly Tyr Val Ser Glu Arg 180 185 190	576
TTC CCC GGC CGC CGG ATA ATA TTG GTG GGG TTC AGT ATG GGC GGC GCT Phe Pro Gly Arg Arg Ile Ile Leu Val Gly Phe Ser Met Gly Gly Ala 195 200 205	624
GTA GCG ATC GTG GAG GGT GCT GGG GAC CCG CGG GTC TAC GCG GTG GCT Val Ala Ile Val Glu Gly Ala Gly Asp Pro Arg Val Tyr Ala Val Ala 210 215 220	672
GCT GAT AGC CCG TAC TAT AGG CTC CGG GAC GTC ATA CCC CGG TGG CTG Ala Asp Ser Pro Tyr Tyr Arg Leu Arg Asp Val Ile Pro Arg Trp Leu 225 230 235 240	720
GAG TAC AAG ACG CCG CTG CCG GGC TGG GTG GGT GTG CTG GCC GGG TTC Glu Tyr Lys Thr Pro Leu Pro Gly Trp Val Gly Val Leu Ala Gly Phe 245 250 255	768
TAC GGG AGG CTG ATG GCG GGC GTT GAC CTC GGC TTC GGC CCC GCT GGG Tyr Gly Arg Leu Met Ala Gly Val Asp Leu Gly Phe Gly Pro Ala Gly 260 265 270	816
GTG GAG CGC GTG GAT AAG CCG TTG CTG GTG GTG TAT GGG CCC CGG GAC Val Gly Arg Val Asp Lys Pro Leu Leu Val Val Tyr Gly Pro Arg Asp 275 280 285	864
CCG CTG GTG ACG CGG GAC GAG GCG AGG AGC CTG GCG TCC CGT AGC CCG Pro Leu Val Thr Arg Asp Glu Ala Arg Ser Leu Ala Ser Arg Ser Pro 290 295 300	912
TGT GGC CGT CTC GTC GAG GTT CCT GGG GCT GGC CAC GTG GAG GCC GTG Cys Gly Arg Leu Val Glu Val Pro Gly Ala Gly His Val Glu Ala Val 305 310 315 320	960
GAT GTG CTC GGG CCG GGC CGC TAC GCA GAC ATG CTG ATA GAG CTG GCG Asp Val Leu Gly Pro Gly Arg Tyr Ala Asp Met Leu Ile Glu Leu Ala 325 330 335	1008
CAC GAG GAG TGC CCT CCG GGG GCC GGT GGC TGA His Glu Glu Cys Pro Pro Gly Ala Gly Gly 340 345	1019

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 789 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG CCA TAT GTT AGG AAT GGT GGT GTA AAT ATC TAT TAT GAA CTG GTG Met Pro Tyr Val Arg Asn Gly Gly Val Asn Ile Tyr Tyr Glu Leu Val 1 5 10 15	48
GAT GGA CCT GAG CCA CCA ATT GTC TTT GTT CAC GGA TGG ACA GCA AAT Asp Gly Pro Glu Pro Pro Ile Val Phe Val His Gly Trp Thr Ala Asn 20 25 30	96
ATG AAT TTT TGG AAA GAG CAA AGA CGT TAT TTT GCA GGC AGG AAT ATG Met Asn Phe Trp Lys Glu Gln Arg Arg Tyr Phe Ala Gly Arg Asn Met 35 40 45	144
ATG TTG TTT GTC GAT AAC AGA GGT CAT GGC AGG TCC GAT AAG CCA CTT Met Leu Phe Val Asp Asn Arg Gly His Gly Arg Ser Asp Lys Pro Leu 50 55 60	192
GGA TAC GAT TTC TAC AGA TTT GAG AAC TTC ATT TCA GAT TTA GAT GCG Gly Tyr Asp Phe Tyr Arg Phe Glu Asn Phe Ile Ser Asp Leu Asp Ala 65 70 75 80	240
GTT GTT AGG GAG ACT GGA GTG GAG AAA TTT GTT CTC GTC GGA CAT TCA Val Val Arg Glu Thr Gly Val Glu Lys Phe Cal Leu Val Gly His Ser 85 90 95	288
TTC GGA ACA ATG ATC TCT ATG AAG TAC TGT TCG GAG TAT CGG AAT CGG Phe Gly Thr Met Ile Ser Met Lys Tyr Cys Ser Glu Tyr Arg Asn Arg 100 105 110	336
GTT CTT GCT CTA ATC CTC ATA GGT GGT GGG AGC AGA ATA AAG CTT CTA Val Leu Ala Leu Ile Leu Ile Gly Gly Ser Arg Ile Lys Leu Leu 115 120 125	384
CAC AGA ATT GGA TAT CCT TTA GCA AAG ATT CTT GCA TCC ATT GCA TAC His Arg Ile Gly Tyr Pro Leu Ala Lys Ile Leu Ala Ser Ile Ala Tyr 130 135 140	432
AAG AAG TCT TCA AGA TTG GTC GCA GAT CTT TCC TTT GGC AAA AAT GCT Lys Lys Ser Ser Arg Leu Val Ala Asp Leu Ser Phe Gly Lys Asn Ala 145 150 155 160	480
GGT GAA CTT AAA GAG TGG GGA TGG AAA CAG GCA ATG GAT TAT ACA CCC Gly Glu Leu Lys Glu Trp Gly Trp Lys Gln Ala Met Asp Tyr Thr Pro 165 170 175	528
TCC TAC GTG GCA ATG GAC ACG TAC AGA ACT CTA ACG AAA GTG AAT CTT Ser Tyr Val Ala Met Tyr Thr Tyr Arg Thr Leu Thr Lys Val Asn Leu 180 185 190	576
GAA AAT ATC TTG GAG AAA ATA GAC TGT CCA ACA CTG ATT ATC GTT GGA Glu Asn Ile Leu Glu Lys Ile Asp Cys Pro Thr Leu Ile Ile Val Gly 195 200 205	624
GAA GAG GAT GCA CTA TTG CCC GTT AGC AAA TCA GTT GAG CTG AGC AGG Glu Glu Asp Ala Leu Leu Pro Val Ser Lys Ser Val Glu Leu Ser Arg 210 215 220	672
AGG ATA GAA AAC TCA AAG CTT GTG ATC ATC CCA AAC TCG GGG CAT TGC Arg Ile Glu Asn Ser Lys Leu Val Ile Ile Pro Asn Ser Gly His Cys 225 230 235 240	720
GTA ATG CTT GAG AGT CCA AGT GAG GTT AAT AGA GCA ATG GAC GAA TTC Val Met Leu Glu Ser Pro Ser Glu Val Asn Arg Ala Met Asp Glu Phe 245 250 255	768

ATT TCT TCA GCA CAG TTC TAA
 Ile Ser Ser Ala Gln Phe
 260

774

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 756 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTG AGA TTG AGG AAA TTT GAA GAG ATA AAC CTC GTT CTT TCG GGA GGA Leu Arg Leu Arg Lys Phe Glu Glu Ile Asn Leu Val Leu Ser Gly Gly 1 5 10 15	48
GCT GCA AAG GGC ATA GCC CAC ATA GGT GTT TTG AAA GCT ATA AAC GAG Ala Ala Lys Gly Ile Ala His Ile Gly Val Leu Lys Ala Ile Asn Glu 20 25 30	96
CTC GGT ATA AGG GTG AGG GCT TTA AGC GGG GTG AGC GCC GGG GCA ATC Leu Glu Ile Arg Val Arg Ala Leu Ser Gly Val Ser Ala Gly Ala Ile 35 40 45	144
GTT TCG GTC TTT TAT GCC TCA GGC TAC TCC CCT GAA GGG ATG TTC AGC Val Ser Val Phe Tyr Ala Ser Gly Tyr Ser Pro Glu Gly Met Phe Ser 50 55 60	192
CTT CTG AAG AGG GTA AAC TGG CTG AAG CTG TTT AAG TTC AAG CCA CCT Leu Leu Lys Arg Val Asn Trp Leu Lys Leu Phe Lys Phe Lys Pro Pro 65 70 75 80	240
CTG AAG GGA TTG ATA GGG TGG GAG AAG GCT ATA AGA TTC CTT GAG GAA Leu Lys Gly Leu Ile Gly Trp Glu Lys Ala Ile Arg Phe Leu Glu Glu 85 90 95	288
GTT CTC CCT TAC AGG AGA ATA GAA AAA CTT GAG ATA CCG ACG TAT ATA Val Leu Pro Tyr Arg Arg Ile Glu Lys Leu Glu Ile Pro Thr Tyr Ile 100 105 110	336
TGC GCG ACG GAT TTA TAC TCG GGA AGG GCT CTA TAC CTC TCG GAA GGG Cys Ala Thr Asp Leu Tyr Ser Gly Arg Ala Leu Tyr Leu Ser Glu Gly 115 120 125	384
AGT TTA ATC CCC GCA CTT CTC GGC AGC TGT GCA ATT CCC GGC ATA TTT Ser Leu Ile Pro Ala Leu Leu Gly Ser Cys Ala Ile Pro Gly Ile Phe 130 135 140	432
GAA CCC GTT GAG TAT AAG AAT TAC TTG CTC GTT GAC GGA GGT ATA GTT Glu Pro Val Glu Tyr Lys Asn Tyr Leu Leu Val Asp Gly Gly Ile Val 145 150 155 160	480
AAC AAC CTT CCC GTT GAG CCC TTT CAG GAA AGC GGT ATT CCC ACC GTT Asn Asn Leu Pro Val Glu Pro Phe Gln Glu Ser Gly Ile Pro Thr Val 165 170 175	528
TGC GTT GAT GTC CTT CCC ATA GAG CCG GAA AAG GAT ATA AAG AAC ATT Cys Val Asp Val Leu Pro Ile Glu Pro Glu Lys Asp Ile Lys Asn Ile 180 185 190	576

CTT CAC ATC CTT TTG AGG AGC TTC TTT CTT GCG GTC CGC TCA AAC TCC	624
Leu His Ile Leu Leu Arg Ser Phe Phe Leu Ala Val Arg Ser Asn Ser	
195 200 205	
GAA AAG AGA AAG GAG TTT TGT GAC CTC GTT ATA GTT CCT GAG CTT GAG	672
Glu Lys Arg Lys Glu Phe Cys Asp Leu Val Ile Val Pro Glu Leu Glu	
210 215 220	
GAG TTC ACA CCC CTT GAT GTT AGA AAA GCG GAC CAA ATA ATG GAG AGG	720
Glu Phe Thr Pro Leu Asp Val Arg Lys Ala Asp Gln Ile Met Glu Arg	
225 230 235 240	
GGA TAC ATA AAG GCC TTA GAG TGA CTT TCT GAA TAG	768
Gly Tyr Ile Lys Ala Leu Glu Val Leu Ser Glu	
245 250	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 894 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG TTT AAT ATC AAT GTC TTT GTT AAT ATA TCT TGG CTG TAT TTT TCA	48
Met Phe Asn Ile Asn Val Phe Val Asn Ile Ser Trp Leu Tyr Phe Ser	
1 5 10 15	
GGG ATA GTT ATG AAG ACT GTG GAA GAG TAT GCG CTA CTT GAA ACA GGC	96
Gly Ile Val Met Lys Thr Val Glu Tyr Ala Leu Leu Glu Thr Gly	
20 25 30	
GTA AGA GTG TTT TAT CGG TGT GTA ATC CCG GAG AAA GCT TTT AAC ACT	144
Val Arg Val Phe Tyr Arg Cys Val Ile Pro Glu Lys Ala Phe Asn Thr	
35 40 45	
TTG ATA ATA GGT TCA CAC GGA TTG GGG GCG CAC AGT GGA ATC TAC ATT	192
Leu Ile Ile Gly Ser His Gly Leu Gly Ala His Ser Gly Ile Tyr Ile	
50 55 60	
AGT GTT GCT GAA GAA TTT GCT AGG CAC GGA TTT GGA TTC TGC ATG CAC	240
Ser Val Ala Glu Glu Phe Ala Arg His Gly Phe Gly Phe Cys Met His	
65 70 75 80	
GAT CAA AGG GGA CAT GGG AGA ACG GCA AGC GAT AGA GAA AGA GGG TAT	288
Asp Gln Arg Gly His Gly Arg Thr Ala Ser Asp Arg Glu Arg Gly Tyr	
85 90 95	
GTG GAG GGC TTT CAC AAC TTC ATA GAG GAT ATG AAG GCC TTC TCC GAT	336
Val Glu Gly Phe His Asn Phe Ile Glu Asp Met Lys Ala Phe Ser Asp	
100 105 110	
TAT GCC AAG TGG CGC GTG GGA GGT GAC GAA ATA ATA TTG CTA GGA CAC	384
Tyr Ala Lys Trp Arg Val Gly Gly Asp Glu Ile Ile Leu Leu Gly His	
115 120 125	
AGT ATG GGC GGG CTG ATA GCG CTC GGA ACA GTT GCA ACT TAT AAA GAA	432
Ser Met Gly Gly Leu Ile Ala Leu Leu Thr Val Ala Thr Tyr Lys Glu	

130	135	140	
ATC GCC AAG GGA GTT ATC GCG CTA GCC CCG GCC CTC CAA ATC CCC TTA			480
Ile Ala Lys Gly Val Ile Ala Leu Ala Pro Ala Leu Gln Ile Pro Leu			
145	150	155	160
ACC CCG GCT AGA AGA CTT GTT CTA AGC CTC GCG TCA AGG CTT GCC CCG			528
Thr Pro Ala Arg Arg Leu Val Leu Ser Leu Ala Ser Arg Leu Ala Pro			
	165	170	175
CAT TCT AAG ATC ACC TTA CAA AGG AGA TTG CCG CAG AAA CCA GAG GGT			576
His Ser Lys Ile Thr Leu Gln Arg Arg Leu Pro Gln Lys Pro Glu Gly			
	180	185	190
TTT CAA AGA GCA AAA GAT ATA GAA TAC AGT CTG AGT GAA ATA TCA GTC			624
Phe Gln Arg Ala Lys Asp Ile Glu Tyr Ser Leu Ser Glu Ile Ser Val			
	195	200	205
AAG CTC GTG GAC GAA ATG ATT AAA GCA TCA TCT ATG TCT TGG ACC ATA			672
Lys Leu Val Asp Glu Met Ile Lys Ala Ser Ser Met Phe Trp Thr Ile			
	210	215	220
GCA GGG GAA ATT AAT ACT CCC GTC CTG CTT ATT CAT GGG GAA AAA CAG			720
Ala Gly Glu Ile Asn Thr Pro Val Leu Leu Ile His Gly Glu Lys Asp			
	225	230	235
AAT GTC ATA CCT CCG GAG GCG AGC AAA AAA GCC RTAC CAA TTA ATA CCT			768
Asn Val Ile Pro Pro Glu Ala Ser Lys Lys Als Tyr Gln Leu Ile Pro			
	245	250	255
TCA TTC CCT AAA GAG TTG AAA AAA TAC CCC GAT CTT GGA CAC AAC TTG			816
Ser Phe Pro Lys Glu Leu Lys Ile Tyr Pro Asp Leu Gly His Asn Leu			
	260	265	270
TTT TTT GAA CCA GGC GCG GTG AAA ATC GTC ACA GAC ATT GTA GAG TGG			864
Phe Phe Glu Pro Gly Ala Val Lys Ile Val Thr Asp Ile Val Glu Trp			
	275	280	285
GTT AAG AAT CTA CCC AGG GAA AAT CCT TAA			874
Val Lys Asn Leu Pro Arg Glu Asn Pro			
	290	295	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 789 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG GAG GTT TAC AAG GCC AAA TTC GGC GAA GCA AAG CTC GGC TGG GTC	48
Met Glu Val Tyr Lys Ala Lys Phe Gly Glu Ala Lys Leu Gly Trp Val	
1 5 10 15	
GTT CTG GTT CAT GGC CTC GGC GAG CAC AGC GGA AGG TAT GGA AGA CTG	96
Val Leu Val His Gly Leu Gly Glu His Ser Gly Arg Tyr Gly Arg Leu	
20 25 30	
ATT AAG GAA CTC AAC TAT GCC GGC TTT GGA GTT TAC ACC TTC GAC TGG	144
Ile Lys Glu Leu Asn Tyr Ala Gly Phe Gly Val Tyr Thr Phe Asp Trp	

35	40	45	
CCC GGC CAC GGG AAG AGC CCG GGC AAG AGA GGG CAC ACG AGC GTC GAG Pro Gly His Gly Lys Ser Pro Gly Lys Arg Gly His Thr Ser Val Glu 50 55 60			192
GAG GCG ATG GAA ATC ATC GAC TCG ATA ATC GAG GAG ATC AGG GAG AAG Glu Ala Met Glu Ile Ile Asp Ser Ile Ile Glu Glu Ile Arg Glu Lys 65 70 75 80			240
CCC TTC CTC TTC GGC CAC AGC CTC GGT GGT CTA ACT GTC ATC AGG TAC Pro Phe Leu Phe Gly His Ser Leu Gly Gly Leu Thr Val Ile Arg Tyr 85 90 95			288
GCT GAG ACG CGG CCC GAT AAA ATA CGG GGA TTA ATA GCT TCC TCG CCT Ala Glu Thr Arg Pro Asp Lys Ile Arg Gly Leu Ile Ala Ser Ser Pro 100 105 110			336
GCC CTC GCC AAG AGC CCG GAA ACG CCG GGC TTC ATG GTG GCC CTC GCG Ala Leu Ala Lys Ser Pro Glu Thr Pro Gly Phe Met Val Ala Leu Ala 115 120 125			384
AAG TTC CTT GGA AAG ATC GCC CCG GGA GTT GTT CTC TCC AAC GGC ATA Lys Phe Leu Gly Lys Ile Ala Pro Gly Val Val Leu Ser Asn Gly Ile 130 135 140			432
AAG CCG GAA CTC CTC TCG AGG AAC AGG GAC GCC GTG AGG AGG TAC GTT Lys Pro Glu Leu Leu Ser Arg Asn Arg Asp Ala Val Arg Arg Tyr Val 145 150 155 160			480
GAA GAC CCA CTC GRC CAC GAC AGG ATT TCG GCC AAG CTG GGA AGG AGC Glu Asp Pro Leu Val His Asp Arg Ile Ser Ala Lys Leu Gly Arg Ser 165 170 175			528
ATC TTC GTG AAC ATG GAG CTG GCC CAC AGG GAG GCG GAC AAG ATA AAA Ile Phe Val Asn Met Glu Leu Ala His Arg Glu Ala Asp Lys Ile Lys 180 185 190			576
GTC CCG ATC CTC CTT CTG ATC GGC ACT GGC GAT GTA ATA ACC CCG CCT Val Pro Ile Leu Leu Leu Ile Gly Thr Gly Asp Val Ile Thr Pro Pro 195 200 205			624
GAA GGC TCA CGC AGA CTC TTC GAG GAG CTG GCC GTC GAG AAC AAA ACC Glu Gly Ser Arg Arg Leu Phe Glu Glu Leu Ala Val Glu Asn Lys Thr 210 215 220			672
CTG AGG GAG TTC GAG GGG GCG TAC CAC GAG ATA TTT GAA GAC CCC GAG Leu Arg Glu Phe Glu Gly Ala Tyr His Glu Ile Phe Glu Asp Pro Glu 225 230 235 240			720
TGG GCC GAG GAG TTC CAC GAA ACA ATT GTT AAG TGG CTG GTT GAA AAA Trp Ala Glu Glu Phe His Glu Thr Ile Val Lys Trp Leu Val Glu Lys 245 250 255			768
TCG TAC TCT TCG GCT CAA TAA Ser Tyr Ser Ser Ala Gln 260			775

- (2) INFORMATION FOR SEQ ID NO:29:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 750 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTG ATT GGC AAT TTG AAA TTG AAG AGG TTT GAA GAG GTT AAC TTA GTT	48
Leu Ile Gly Asn Leu Lys Ley Lys Arg Phe Glu Glu Val Asn Leu Val	
1 5 10 15	
CTT TCG GGA GGG GCT GCC AAG GGT ATC GCC CAT ATA GGT GTT TTA AAA	96
Leu Ser Gly Gly Ala Ala Lys Gly Ile Ala His Ile Gly Val Leu Lys	
20 25 30	
GCT CTG GAA GAG CTC GGT ATA AAG GTA AAG AGG CTC AGC GGG GTA AGT	144
Ala Leu Glu Glu Leu Gly Ile Lys Val Lys Arg Leu Ser Gly Val Ser	
35 40 45	
GCT GGA GCT ATC GTT TCC GTC TTT TAC GCT TCG GGC TAC ACT CCC GAC	192
Ala Gly Ala Ile Val Ser Val Phe Tyr Ala Ser Gly Tyr Thr Pro Asp	
50 55 60	
GAG ATG TTA AAA CTC CTG AAA GAG GTA AAC TGG CTC AAA CTT TTT AAG	240
Glu Met Leu Lys Leu Leu Lys Glu Val Asn Trp Leu Lys Leu Phe Lys	
65 70 75 80	
TTC AAA ACA CCG AAA ATG GGC TTA ATG GGG TGG GAG AAG GCT GCA GAG	288
Phe Lys Thr Pro Lys Met Gly Leu Met Gly Trp Glu Lys Ala Ala Glu	
85 90 95	
TTT TTG TAA AAA GAG CTC GGA GTT AAG AGG CTG GAA GAC CTG AAC ATA	336
Phe Leu Glu Lys Glu Leu Gly Val Lys Arg Leu Glu Asp Leu Asn Ile	
100 105 110	
CCA ACC TAT CTT TGC TCG GCG GAT CTG TAC ACG GGA AAG GCT CTT TAC	384
Pro Thr Tyr Leu Cys Ser Ala Asp Ley Tyr Thr Gly Lys Ala Leu Tyr	
115 120 125	
TTC GGC AGA GGT GAC TTA ATT CCC GTG CTT CTC GGA AGT TGT TCC ATA	432
Phe Gly Arg Gly Asp Leu Ile Pro Val Leu Leu Gly Ser Lys Ser Ile	
130 135 140	
CCC GGG ATT TTT GAA CCA GTT GAG TAC GAG AAT TTT CTA CTT GTT GAC	480
Pro Gly Ile Phe Glu Pro Val Glu Tyr Glu Asn Phe Leu Leu Val Asp	
145 150 155 160	
GGA GGT ATA GTG AAC AAC CTG CCC GTA GAA CCT TTG GAA AAG TTC AAA	528
Gly Gly Ile Val Asn Asn Leu Pro Val Glu Pro Leu Glu Lys Phe Lys	
165 170 175	
GAA CCC ATA ATC GGG GTA GAT GTG CTT CCC ATA ACT CAA GAA AGA AAG	576
Glu Pro Ile Ile Gly Val Asp Val Leu Pro Ile Thr Gln Glu Arg Lys	
180 185 190	
ATT AAA AAT ATA CTC CAC ATC CTT ATA AGG AGC TTC TTT CTG GCG GTT	624
Ile Lys Asn Ile Leu His Ile Leu Ile Arg Ser Phe Phe Leu Ala Val	
195 200 205	
CGT TCC AAT TCG GAA AAG AGA AAG GAG TTC TGC AAC GTA GTT ATA GAA	672
Arg Ser Asn Ser Glu Lys Arg Lys Glu Phe Cys Asn Val Val Ile Glu	
210 215 220	
CCT CCC CTT GAA GAG TTC TCT CCT CTG GAC GTA AAT AAG GCG GAC GAG	720
Pro Pro Leu Glu Glu Phe Ser Pro Leu Asp Val Asn Lys Ala Asp Glu	

225

230

235

240

ATA TTC TGC GGG GAT ATG AGA GCA CTT TAA
 Ile Phe Cys Gly Asp Met Arg Ala Leu
 245

730

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1017 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATG CCA GCT AAT GAC TCA CCC ACG ATC GAC TTT AAT CCT CGC GGC ATT	48
Met Pro Ala Asn Asp Ser Pro Thr Ile Asp Phe Asn Pro Arg Gly Ile	
1 5 10 15	
CTT CGC AAC GCT CAC GCA CAG GTT ATT TTA GCG ACT TCC GGC TTG CGC	96
Leu Arg Asn Ala His Ala Gln Val Ile Leu Ala Thr Ser Gly Leu Arg	
20 25 30	
AAA GCG TTT TTG AAA CGC ACG CAC AAG AGC TAC CTC AGC ACT GCC CAA	144
Lys Ala Phe Leu Lys Arg Thr His Lys Ser Tyr Leu Ser Thr Ala Gln	
35 40 45	
TGG CTG GAG CTC GAT GCC GGC AAC GGA GTT ACC TTG GCC GGA GAG CTT	192
Trp Leu Glu Leu Asp Ala Gly Asn Gly Val Thr Leu Ala Gly Glu Leu	
50 55 60	
AAC ACA GCG CCT GCA ACT GCA TCC TCC TCC CAC CCG GCG CAC AAG AAC 240	
Asn Thr Ala Pro Ala Thr Ala Ser Ser Ser His Pro Ala His Lys Asn	
65 70 75 80	
ACT CTG GTT ATT GTG CTG CAC GGC TGG GAA GGC TCC AGC CAG TCG GCC	288
Thr Leu Val Ile Val Leu His Gly Trp Glu Gly Ser Ser Gln Ser Ala	
85 90 95	
TAT GCG ACC TCC GCT GGC AGC ACG CTT TTC GAC AAT GGG TTC GAC ACT	336
Tyr Ala Thr Ser Ala Gly Ser Thr Leu Phe Asp Asn Gly Phe Asp Thr	
100 105 110	
TTT CGC CTT AAT TTT CGC GAT CAC GGC GAC ACC TAC CAC TTA AAC CGC	384
Phe Arg Leu Asn Phe Arg Asp His Gly Asp Thr Tyr His Leu Asn Arg	
115 120 125	
GGC ATA TTT AAC TCA TCG CTG ATT GAC GAA GTA GTG GGC GCA GTC AAA	432
Gly Ile Phe Asn Ser Ser Leu Ile Asp Glu Val Val Gly Ala Val Lys	
130 135 140	
GCC ATC CAG CAG CAA ACC GAC TAC GAC AAG TAT TGC CTG ATG GGG TTC	480
Ala Ile Gln Gln Gln Thr Asp Tyr Asp Lys Tyr Cys Leu Met Gly Phe	
145 150 155 160	
TCA CTG GGT GGG AAC TTT GCC TTG CGC GTC GCG GTG CGG GAA CAG CAT	528
Ser Leu Gly Gly Asn Phe Ala Leu Arg Val Ala Val Arg Glu Gln His	
165 170 175	

CTC GCT AAA CCG CTA GCG GGC GTG CTC GCC GTA TGC CCG GTA CTC GAC Leu Ala Lys Pro Leu Ala Gly Val Leu Ala Val Cys Pro Val Leu Asp 180 185 190	576
CCC GCA CAC ACC ATG ATG GCC CTA AAC CGA GGT GCG TTT TTC TAC GGC Pro Ala His Thr Met Met Ala Leu Asn Arg Gly Ala Phe Phe Tyr Gly 195 200 205	624
CGC TAT TTT GCG CAT AAA TGG AAG CGC TCG TTA ACC GCA AAA CTT GCA Arg Tyr Phe Ala His Lys Trp Lys Arg Ser Leu Thr Ala Lys Leu Ala 210 215 220 225	672
GCT TTC CCA GAC TAC AAA TAC GGC AAA GAT TTA AAA TCG ATA CAC ACG Ala Phe Pro Asp Tyr Lys Tyr Gly Lys Asp Leu Lys Ser Ile His Thr 230 235 240	720
CTT GAT GAG TTA AAC AAC TAT TTC ATT CCC CGC TAC ACC GGC TTC AAC Leu Asp Glu Leu Asn Asn Tyr Phe Ile Pro Arg Tyr Thr Gly Phe Asn 245 250 255	768
TCA GTC TCC GAA TAC TTC AAA AGT TAC ACG CTC ACC GGG CAG AAG CTC Ser Val Ser Glu Tyr Phe Lys Ser Tyr Thr Leu Thr Gly Gln Lys Leu 260 265 270	816
GCG TTT CTC AAC TGC CCC AGT TAC ATT CTG GCA GCT GGC GAC GAC CCA Ala Phe Leu Asn Cys Pro Ser Tyr Ile Leu Ala Ala Gly Asp Asp Pro 275 280 285	864
ATA ATT CCA GCA TCC GAC TTT CAG AAA ATA GCC AAG CCT GCG AAT CTG Ile Ile Pro Ala Ser Asp Phe Gln Lys Ile Ala Lys Pro Ala Asn Leu 290 295 300 305	912
CAC ATA ACA GTA ACG CAA CAA GGT TCT CAT TGC GCA TAC CTG GAA AAC His Ile Thr Val Thr Gln Gln Gly Ser His Cys Ala Tyr Leu Glu Asn 310 315 320	960
CTG CAT AAA CCT AGT GCT GCC GAC AAA TAT GCG GTG AAA TTA TTT GGA Leu His Lys Pro Ser Ala Ala Asp Lys Tyr Ala Val Lys Leu Phe Gly 325 330 335	1,008
GCC TGT TGA Ala Cys	1,111

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 936 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATG CTT GAT ATG CCA ATC GAC CCT GTT TAC TAC CAG CTT GCT GAG TAT Met Leu Asp Met Pro Ile Asp Pro Val Tyr Tyr Gln Leu Ala Glu Tyr 1 5 10 15	48
TTC GAC AGT CTG CCG AAG TTC GAC CAG TTT TCC TCG GCC AGA GAG TAC Phe Asp Ser Leu Pro Lys Phe Asp Gln Phe Ser Ser Ala Arg Glu Tyr 20 25 30	96
AGG GAG GCG ATA AAT CGA ATA TAC GAG GAG AGA AAC CGG CAG CTG AGC	144

Arg	Glu	Ala	Ile	Asn	Arg	Ile	Tyr	Glu	Glu	Arg	Asn	Arg	Gln	Leu	Ser	
		35					40					45				
CAG	CAT	GAG	AGG	GTT	GAA	AGA	GTT	GAG	GAC	AGG	ACG	ATT	AAG	GGG	AGG	192
Gln	His	Glu	Arg	Val	Glu	Arg	Val	Glu	Asp	Arg	Thr	Ile	Lys	Gly	Arg	
		50				55				60						
AAC	GGA	GAC	ATC	AGA	GTC	AGA	GTT	TAC	CAG	CAG	AAG	CCC	GAT	TCC	CCG	240
Asn	Gly	Asp	Ile	Arg	Val	Arg	Val	Tyr	Gln	Gln	Lys	Pro	Asp	Ser	Pro	
	65				70				75						80	
GGT	CTG	GTT	TAC	TAT	CAC	GGT	GGT	GGA	TTT	GTG	ATT	TGC	AGC	ATC	GAG	288
Val	Leu	Val	Tyr	Tyr	His	Gly	Gly	Gly	Phe	Val	Ile	Cys	Ser	Ile	Glu	
				85				90						95		
TCG	CAC	GAC	GCC	TTA	TGC	AGG	AGA	AYY	GCG	AGA	CTT	TCA	AAC	TCT	ACC	336
Ser	His	Asp	Ala	Leu	Cys	Arg	Arg	Ile	Ala	Arg	Leu	Ser	Asn	Ser	Thr	
			100					105					110			
GTA	GTC	TCC	GTG	GAT	TAC	AGG	CTC	GCT	CCT	GAG	CAC	AAG	TTT	CCC	CCC	384
Val	Val	Ser	Val	Asp	Tyr	Arg	Leu	Ala	Pro	Glu	His	Lys	Phe	Pro	Ala	
			115				120					125				
CCA	GTT	TAT	CAT	TGC	TAC	GAT	GCG	ACC	AAG	TGG	GTT	GCT	GAG	AAC	CGG	432
Ala	Val	Tyr	Asp	Cys	Tyr	Aso	Ala	Thr	Lys	Trp	Val	Ala	Glu	Asn	Ala	
			130			135					140					
GAG	GAG	CTG	AGG	ATT	GAC	CCG	TCA	AAA	ATC	TTC	GTT	GGG	GGG	GAC	AGT	480
Glu	Glu	Leu	Arg	Ile	Asp	Pro	Ser	Lys	Ile	Phe	Val	Gly	Gly	Asp	Ser	
					150				155						160	
GCG	GGA	CGG	AAT	CTT	GCC	CCG	GCG	CTT	TCA	ATA	ATG	GCG	AGA	GAC	AGC	528
Ala	Gly	Gly	Asn	Leu	Ala	Ala	Ala	Val	Ser	Ile	Met	Ala	Arg	Asp	Ser	
				165				170						175		
GGA	GAA	GAT	TTC	ATA	AAG	CAT	CAA	ATT	CTA	ACT	TAC	CCC	GTT	GTG	AAC	576
Gly	Glu	Asp	Phe	Ile	Lys	His	Gln	Ile	Leu	Ile	Tyr	Pro	Val	Val	Asn	
			180				185					190				
TTT	GTA	GCC	CCC	ACA	CCA	TCG	CTT	CTG	GAG	TTT	GGA	GAG	GGG	CTG	TGG	624
Phe	Val	Ala	Pro	Thr	Pro	Ser	Leu	Leu	Glu	Phe	Gly	Glu	Gly	Leu	Trp	
		195					200					205				
ATT	CTC	GAC	CAG	AAG	ATA	ATG	AGT	TGG	TTC	TCG	GAG	CAG	TAC	TTC	TCC	672
Ile	Leu	Asp	Gln	Lys	Ile	Met	Ser	Trp	Phe	Ser	Glu	Gln	Tyr	Phe	Ser	
		210				215					230					
AGA	GAG	GAA	GAT	AAG	TTC	AAG	CCC	CTC	GCC	TCC	GTA	ATC	TTT	GCG	GAC	720
Arg	Glu	Glu	Aso	Lys	Phe	Asn	Pro	Leu	Ala	Ser	Val	Ile	Phe	Ala	Asp	
					240				245						250	
CTT	GAG	AAC	CTA	CCT	CCT	GCG	CTG	ATC	ATA	ACC	GCC	GAA	TAC	GAC	CCG	768
Leu	Glu	Asn	Leu	Pro	Pro	Ala	Leu	Ile	Ile	Thr	Ala	Glu	Tyr	Asp	Pro	
				255				260						265		
CTG	AGA	GAT	GAA	GGA	GAA	GTT	TTC	GGG	CAG	ATG	CTG	AGA	AGA	GCC	GGT	816
Leu	Arg	Asp	Glu	Gly	Glu	Val	Phe	Gly	Gln	Met	Leu	Arg	Arg	Ala	Gly	
			270				275					280				
GTT	GAG	GCG	AGC	ATC	GTC	AGA	TAC	AGA	GGC	GTG	CTT	CAC	GGA	TTC	ATC	864
Val	Glu	Ala	Ser	Ile	Val	Arg	Tyr	Arg	Gly	Val	Leu	His	Gly	Phe	Ile	
			285				290					295				
AAT	TAC	TAT	CCC	GTG	CTG	AAG	GCT	GCG	AGG	GAT	GCG	ATA	AAC	CAG	ATT	912
Asn	Tyr	Tyr	Pro	Val	Leu	Lys	Ala	Ala	Arg	Asp	Ala	Ile	Asn	Gln	Ile	

300	305	310	
GCC GCT CTT CTT GTG TTC GAC TAG			936
Ala Ala Leu leu Val Phe Asp			
315	320		

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 918 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATG CCC CTA GAT CCT AGA ATT AAA AAG TTA CTA GAA TCA GCT CTT ACT	48
Met Pro Leu Asp Pro Arg Ile Lys Lys Leu Leu Glu Ser Ala Leu Thr	
5 10 15	
ATA CCA ATT GGT AAA GCC CCA GTA GAA GAG GTA AGA AAG ATA TTT AGG	96
Ile Pro Ile Gly Lys Ala Pro Val Glu Glu Val Arg Lys Ile Phe Arg	
20 25 30	
CAA TTA GCG TCG GCA GCT CCC AAA GTC GAA GTT GGA AAA GTA GAA GAT	144
Gln Leu Ala Ser Ala Ala Pro Lys Val Glu Val Gly Lys Val Glu Asp	
35 40 45	
ATA AAA ATA CCA GGC AGT GAA ACC GTT ATA AAC GCT AGA GTG TAT TTT	192
Ile Lys Ile Pro Gly Ser Glu Thr Val Ile Asn Ala Arg Val Tyr Phe	
50 55 60	
CCG AAG AGT AGC GGT CCT TAT GGT GTT CTA GTG TAT CTT CAT GGA GGC	240
Pro Lys Ser Ser Gly Pro Tyr Gly Val Leu Val Tyr Leu His Gly Gly	
65 70 75 80	
GGT TTT GTA ATA GGC GAT GTG GAA TCT TAT GAC CCA TTA TGT AGA GCA	288
Gly Phe Val Ile Gly Asp Val Glu Ser Tyr Asp Pro Leu Cys Arg Ala	
85 90 95	
ATT ACA AAT GCG TGC AAT TGC GTT GTA GTA TCA GTG GAC TAT AGG TTA	336
Ile Thr Asn Ala Cys Asn Cys Val Val Val Ser Val Asp Tyr Arg Leu	
100 105 110	
GCT CCA GAA TAC AAG TTT CCT TCT GCA GTT ATC GAT TCA TTT GAC GCT	384
Ala Pro Glu Tyr Lys Phe Pro Ser Ala Val Ile Asp Ser Phe Asp Ala	
115 120 125	
ACT AAT TGG GTT TAT AAC AAT TTA GAT AAA TTT GAT GGA AAG ATG GGA	432
Thr Asn Trp Val Tyr Asn Asn Leu Asp Lys Phe Asp Gly Lys Met Gly	
130 135 140	
GTT GCG ATT GCG GGA GAT AGT GCT GGA GGA AAT TTG GCA GCG GTT GTA	480
Val Ala Ile Ala Gly Asp Ser Ale Gly Gly Asn Leu Ala Ala Val Val	
145 150 155 160	
GCT CTT CTT TCA AAG GGT AAA ATT AAT TTG AAG TAT CAA ATA CTG GTT	528
Ala Leu Leu Ser Lys Gly Lys Ile Asn Leu Lys Tyr Gln Ile Leu Val	
165 170 175	
TAC CCA GCG GTA AGT TTA GAT AAC GTT TCA AGA TCC ATG ATA GAG TAC	576

Tyr	Pro	Ala	Val	Ser	Leu	Asp	Asn	Val	Ser	Arg	Ser	Met	Ile	Glu	Tyr		
			180					185					190				
TCT	GAT	GGG	TTC	TTC	CTT	ACC	AGA	GAG	CAT	ATA	GAG	TGG	TTC	GGT	TCT	624	
Ser	Asp	Gly	Phe	Phe	Leu	Thr	Arg	Glu	His	Ile	Glu	Trp	Phe	Gly	Ser		
		195					200					205					
CAA	TAC	TTA	CGA	AGC	CCT	GCA	GAT	TTG	CTA	GAC	TTT	AGG	TTC	TCT	CCA	672	
Gln	Tyr	Leu	Arg	Ser	Pro	Ala	Asp	Leu	Leu	Asp	Phe	Arg	Phe	Ser	Pro		
	210					215					220						
ATT	CTG	GCG	CAA	GAT	TTC	AAC	GGA	TTA	CCT	CCA	GCC	TTG	ATA	ATA	ACA	720	
Ile	Leu	Ala	Gln	Asp	Phe	Asn	Gly	Leu	Pro	Pro	Ala	Leu	Ile	Ile	Thr		
	225				230					235					240		
GCA	GAA	TAC	GAT	CCA	CTA	AGG	GAT	CAA	GGA	GAA	GCG	TAT	GCA	AAT	AAA	768	
Ala	Glu	Tyr	Asp	Pro	Leu	Arg	Asp	Gln	Gly	Glu	Ala	Tyr	Ala	Asn	Lys		
				245					250					255			
CTA	CTA	CAA	GCT	GGA	GTC	TCA	GTT	ACT	AGT	GTG	AGA	TTT	AAC	AAC	GTT	816	
Leu	Leu	Gln	Ala	Gly	Val	Ser	Val	Thr	Ser	Val	Arg	Phe	Asn	Asn	Val		
			260					265					270				
ATA	CAC	GGA	TTC	CTC	TCA	TTC	TTT	CCG	TTG	ATG	GAG	CAA	GGA	AGA	GAT	864	
Ile	His	Gly	Phe	Leu	Ser	Phe	Phe	Pro	Leu	Met	Glu		Gly	Arg	Asp		
		275					280					285					
GCT	ATA	GGT	CTG	ATA	GGG	TCT	GTG	TTA	AGA	CGA	GTA	TTT	TAT	GAT	AAA	912	
Ala	Ile	Gly	Leu	Ile	Gly	Ser	Val	Leu	Arg	Arg	Val	Phe	Tyr	Asp	Lys		
	290					295					300						
ATT	TAA															918	
Ile																	
305																	

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 184 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ser	Leu	Asn	Lys	His	Ser	Trp	Met	Asp	Met	Ile	Ile	Phe	Ile	Leu		
1				5				10						15			
Ser	Phe	Ser	Phe	Pro	Leu	Thr	Met	Ile	Ala	Leu	Ala	Ile	Ser	Met	Ser		
			20				25						30				
Ser	Trp	Phe	Asn	Ile	Trp	Asn	Asn	Ala	Leu	Ser	Asp	Leu	Gly	His	Ala		
		35				40						45					
Val	Lys	Ser	Ser	Val	Ala	Pro	Ile	Phe	Asn	Leu	Gly	Leu	Ala	Ile	Gly		
	50					55					60						
Gly	Ile	Leu	Ile	Val	Ile	Val	Gly	Leu	Arg	Asn	Leu	Tyr	Ser	Trp	Ser		
	65			70				75						80			
Arg	Val	Lys	Gly	Ser	Leu	Ile	Ile	Ser	Met	Gly	Val	Phe	Leu	Asn	Leu		
				85				90						95			

Ile Gly Val Phe Asp Glu Val Tyr Gly Trp Ile His Phe Leu Val Ser
100 105 110
Val Leu Phe Phe Leu Ser Ile Ile Ala Tyr Phe Ile Ala Ile Ser Ile
115 120 125
Leu Asp Lys Ser Trp Ile Ala Val Leu Leu Ile Ile Gly His Ile Ala
130 135 140
Met Trp Tyr Leu His Phe Ala Ser Glu Ile Pro Arg Gly Ala Ala Ile
145 150 155 160
Pro Glu Leu Leu Ala Val Phe Ser Phe Leu Pro Phe Tyr Ile Arg Asp
165 170 175
Tyr Phe Lys Ser Tyr Thr Lys Arg
180

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 346 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Lys Leu Leu Glu Pro Thr Asn Thr Ser Tyr Thr Leu Leu Gln Asp
1 5 10 15
Leu Ala Leu His Phe Ala Phe Tyr Trp Phe Leu Ala Val Tyr Thr Trp
20 25 30
Leu Pro Gly Val Leu Val Arg Gly Val Ala Val Asp Thr Gly Val Ala
35 40 45
Arg Val Pro Gly Leu Gly Arg Arg Gly Lys Arg Leu Leu Leu Ala Ala
50 55 60
Val Ala Val Leu Ala Leu Val Val Ser Val Val Val Pro Ala Tyr Val
65 70 75 80
Ala Tyr Ser Ser Leu His Pro Glu Ser Cys Arg Pro Val Ala Pro Glu
85 90 95
Gly Leu Thr Tyr Lys Glu Phe Ser Val Thr Ala Glu Asp Gly Leu Val
100 105 110
Val Arg Gly Trp Cal Leu Gly Pro Gly Ala Gly Gly Asn Pro Val Phe
115 120 125
Val Leu Met His Gly Tyr Thr Gly Cys Arg Ser Ala Pro Tyr Met Ala
130 135 140
Val Leu Ala Arg Glu Leu Val Glu Trp Gly Tyr Pro Val Val Val Phe
145 150 155 160
Asp Phe Arg Gly His Gly Glu Ser Gly Gly Ser Thr Thr Ile Gly Pro
165 170 175
Arg Glu Val Leu Asp Ala Arg Ala Val Val Gly Tyr Val Ser Glu Arg
180 185 190

Phe Pro Gly Arg Arg Ile Ile Leu Val Gly Phe Ser Met Gly Gly Ala
 195 200 205
 Val Ala Ile Val Glu Gly Ala Gly Asp Pro Arg Val Tyr Ala Val Ala
 210 215 220
 Ala Asp Ser Pro Tyr Tyr Arg Leu Arg Asp Val Ile Pro Arg Trp Leu
 225 230 235 240
 Glu Tyr Lys Thr Pro Leu Pro Gly Trp Val Gly Val Leu Ala Gly Phe
 245 250 255
 Tyr Gly Arg Leu Met Ala Gly Val Asp Leu Gly Phe Gly Pro Ala Gly
 260 265 270
 Val Gly Arg Val Asp Lys Pro Leu Leu Val Val Tyr Gly Pro Arg Asp
 275 280 285
 Pro Leu Val Thr Arg Asp Glu Ala Arg Ser Leu Ala Ser Arg Ser Pro
 290 295 300
 Cys Gly Arg Leu Val Glu Val Pro Gly Ala Gly His Val Glu Ala Val
 305 310 315 320
 Asp Val Leu Gly Pro Gly Arg Tyr Ala Asp Met Leu Ile Glu Leu Ala
 325 330 335
 His Glu Glu Cys Pro Pro Gly Ala Gly Gly
 340 345

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 262 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Pro Tyr Val Arg Asn Gly Gly Val Asn Ile Tyr Tyr Glu Leu Val
 1 5 10 15
 Asp Gly Pro Glu Pro Pro Ile Val Phe Val His Gly Trp Thr Ala Asn
 20 25 30
 Met Asn Phe Trp Lys Glu Gln Arg Arg Tyr Phe Ala Gly Arg Asn Met
 35 40 45
 Met Leu Phe Val Asp Asn Arg Gly His Gly Arg Ser Asp Lys Pro Leu
 50 55 60
 Gly Tyr Asp Phe Tyr Arg Phe Glu Asn Phe Ile Ser Asp Leu Asp Ala
 65 70 75 80
 Val Val Arg Glu Thr Gly Val Glu Lys Phe Cal Leu Val Gly His Ser
 85 90 95
 Phe Gly Thr Met Ile Ser Met Lys Tyr Cys Ser Glu Tyr Arg Asn Arg
 100 105 110
 Val Leu Ala Leu Ile Leu Ile Gly Gly Gly Ser Arg Ile Lys Leu Leu

115 120 125
 His Arg Ile Gly Tyr Pro Leu Ala Lys Ile Leu Ala Ser Ile Ala Tyr
 130 135 140
 Lys Lys Ser Ser Arg Leu Val Ala Asp Leu Ser Phe Gly Lys Asn Ala
 145 150 155 160
 Gly Glu Leu Lys Glu Trp Gly Trp Lys Gln Ala Met Asp Tyr Thr Pro
 165 170 175
 Ser Tyr Val Ala Met Tyr Thr Tyr Arg Thr Leu Thr Lys Val Asn Leu
 180 185 190
 Glu Asn Ile Leu Glu Lys Ile Asp Cys Pro Thr Leu Ile Ile Val Gly
 195 200 205
 Glu Glu Asp Ala Leu Leu Pro Val Ser Lys Ser Val Glu Leu Ser Arg
 210 215 220
 Arg Ile Glu Asn Ser Lys Leu Val Ile Ile Pro Asn Ser Gly His Cys
 225 230 235 240
 Val Met Leu Glu Ser Pro Ser Glu Val Asn Arg Ala Met Asp Glu Phe
 245 250 255
 Ile Ser Ser Ala Gln Phe
 260

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 251 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Arg Leu Arg Lys Phe Glu Glu Ile Asn Leu Val Leu Ser Gly Gly
 1 5 10 15
 Ala Ala Lys Gly Ile Ala His Ile Gly Val Leu Lys Ala Ile Asn Glu
 20 25 30
 Leu Glu Ile Arg Val Arg Ala Leu Ser Gly Val Ser Ala Gly Ala Ile
 35 40 45
 Val Ser Val Phe Tyr Ala Ser Gly Tyr Ser Pro Glu Gly Met Phe Ser
 50 55 60
 Leu Leu Lys Arg Val Asn Trp Leu Lys Leu Phe Lys Phe Lys Pro Pro
 65 70 75 80
 Leu Lys Gly Leu Ile Gly Trp Glu Lys Ala Ile Arg Phe Leu Glu Glu
 85 90 95
 Val Leu Pro Tyr Arg Arg Ile Glu Lys Leu Glu Ile Pro Thr Tyr Ile
 100 105 110
 Cys Ala Thr Asp Leu Tyr Ser Gly Arg Ala Leu Tyr Leu Ser Glu Gly
 115 120 125

Ser Leu Ile Pro Ala Leu Leu Gly Ser Cys Ala Ile Pro Gly Ile Phe
130 135 140

Glu Pro Val Glu Tyr Lys Asn Tyr Leu Leu Val Asp Gly Gly Ile Val
145 150 155 160

Asn Asn Leu Pro Val Glu Pro Phe Gln Glu Ser Gly Ile Pro Thr Val
165 170 175

Cys Val Asp Val Leu Pro Ile Glu Pro Glu Lys Asp Ile Lys Asn Ile
180 185 190

Leu His Ile Leu Leu Arg Ser Phe Phe Leu Ala Val Arg Ser Asn Ser
195 200 205

Glu Lys Arg Lys Glu Phe Cys Asp Leu Val Ile Val Pro Glu Leu Glu
210 215 220

Glu Phe Thr Pro Leu Asp Val Arg Lys Ala Asp Gln Ile Met Glu Arg
225 230 235 240

Gly Tyr Ile Lys Ala Leu Glu Val Leu Ser Glu
245 250

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 297 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Phe Asn Ile Asn Val Phe Val Asn Ile Ser Trp Leu Tyr Phe Ser
1 5 10 15

Gly Ile Val Met Lys Thr Val Glu Glu Tyr Ala Leu Leu Glu Thr Gly
20 25 30

Val Arg Val Phe Tyr Arg Cys Val Ile Pro Glu Lys Ala Phe Asn Thr
35 40 45

Leu Ile Ile Gly Ser His Gly Leu Gly Ala His Ser Gly Ile Tyr Ile
50 55 60

Ser Val Ala Glu Glu Phe Ala Arg His Gly Phe Gly Phe Cys Met His
65 70 75 80

Asp Gln Arg Gly His Gly Arg Thr Ala Ser Asp Arg Glu Arg Gly Tyr
85 90 95

Val Glu Gly Phe His Asn Phe Ile Glu Asp Met Lys Ala Phe Ser Asp
100 105 110

Tyr Ala Lys Trp Arg Val Gly Gly Asp Glu Ile Ile Leu Leu Gly His
115 120 125

Ser Met Gly Gly Leu Ile Ala Leu Leu Thr Val Ala Thr Tyr Lys Glu
130 135 140

Ile Ala Lys Gly Val Ile Ala Leu Ala Pro Ala Leu Gln Ile Pro Leu
145 150 155 160

Thr Pro Ala Arg Arg Leu Val Leu Ser Leu Ala Ser Arg Leu Ala Pro
 165 170 175
 His Ser Lys Ile Thr Leu Gln Arg Arg Leu Pro Gln Lys Pro Glu Gly
 180 185 190
 Phe Gln Arg Ala Lys Asp Ile Glu Tyr Ser Leu Ser Glu Ile Ser Val
 195 200 205
 Lys Leu Val Asp Glu Met Ile Lys Ala Ser Ser Met Phe Trp Thr Ile
 210 215 220
 Ala Gly Glu Ile Asn Thr Pro Val Leu Leu Ile His Gly Glu Lys Asp
 225 230 235 240
 Asn Val Ile Pro Pro Glu Ala Ser Lys Lys Als Tyr Gln Leu Ile Pro
 245 250 255
 Ser Phe Pro Lys Glu Leu Lys Ile Tyr Pro Asp Leu Gly His Asn Leu
 260 265 270
 Phe Phe Glu Pro Gly Ala Val Lys Ile Val Thr Asp Ile Val Glu Trp
 275 280 285
 Val Lys Asn Leu Pro Arg Glu Asn Pro
 290 295

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 262 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Glu Val Tyr Lys Ala Lys Phe Gly Glu Ala Lys Leu Gly Trp Val
 1 5 10 15
 Val Leu Val His Gly Leu Gly Glu His Ser Gly Arg Tyr Gly Arg Leu
 20 25 30
 Ile Lys Glu Leu Asn Tyr Ala Gly Phe Gly Val Tyr Thr Phe Asp Trp
 35 40 45
 Pro Gly His Gly Lys Ser Pro Gly Lys Arg Gly His Thr Ser Val Glu
 50 55 60
 Glu Ala Met Glu Ile Ile Asp Ser Ile Ile Glu Glu Ile Arg Glu Lys
 65 70 75 80
 Pro Phe Leu Phe Gly His Ser Leu Gly Gly Leu Thr Val Ile Arg Tyr
 85 90 95
 Ala Glu Thr Arg Pro Asp Lys Ile Arg Gly Leu Ile Ala Ser Ser Pro
 100 105 110
 Ala Leu Ala Lys Ser Pro Glu Thr Pro Gly Phe Met Val Ala Leu Ala
 115 120 125
 Lys Phe Leu Gly Lys Ile Ala Pro Gly Val Val Leu Ser Asn Gly Ile

130 135 140
 Lys Pro Glu Leu Leu Ser Arg Asn Arg Asp Ala Val Arg Arg Tyr Val
 145 150 155 160
 Glu Asp Pro Leu Val His Asp Arg Ile Ser Ala Lys Leu Gly Arg Ser
 165 170 175
 Ile Phe Val Asn Met Glu Leu Ala His Arg Glu Ala Asp Lys Ile Lys
 180 185 190
 Val Pro Ile Leu Leu Leu Ile Gly Thr Gly Asp Val Ile Thr Pro Pro
 195 200 205
 Glu Gly Ser Arg Arg Leu Phe Glu Glu Leu Ala Val Glu Asn Lys Thr
 210 215 220
 Leu Arg Glu Phe Glu Gly Ala Tyr His Glu Ile Phe Glu Asp Pro Glu
 225 230 235 240
 Trp Ala Glu Glu Phe His Glu Thr Ile Val Lys Trp Leu Val Glu Lys
 245 250 255
 Ser Tyr Ser Ser Ala Gln
 260

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 249 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Leu Ile Gly Asn Leu Lys Ley Lys Arg Phe Glu Glu Val Asn Leu Val
 1 5 10 15
 Leu Ser Gly Gly Ala Ala Lys Gly Ile Ala His Ile Gly Val Leu Lys
 20 25 30
 Ala Leu Glu Glu Leu Gly Ile Lys Val Lys Arg Leu Ser Gly Val Ser
 35 40 45
 Ala Gly Ala Ile Val Ser Val Phe Tyr Ala Ser Gly Tyr Thr Pro Asp
 50 55 60
 Glu Met Leu Lys Leu Leu Lys Glu Val Asn Trp Leu Lys Leu Phe Lys
 65 70 75 80
 Phe Lys Thr Pro Lys Met Gly Leu Met Gly Trp Glu Lys Ala Ala Glu
 85 90 95
 Phe Leu Glu Lys Glu Leu Gly Val Lys Arg Leu Glu Asp Leu Asn Ile
 100 105 110
 Pro Thr Tyr Leu Cys Ser Ala Asp Ley Tyr Thr Gly Lys Ala Leu Tyr
 115 120 125
 Phe Gly Arg Gly Asp Leu Ile Pro Val Leu Leu Gly Ser Lys Ser Ile
 130 135 140

Pro Gly Ile Phe Glu Pro Val Glu Tyr Glu Asn Phe Leu Leu Val Asp
 145 150 155 160
 Gly Gly Ile Val Asn Asn Leu Pro Val Glu Pro Leu Glu Lys Phe Lys
 165 170 175
 Glu Pro Ile Ile Gly Val Asp Val Leu Pro Ile Thr Gln Glu Arg Lys
 180 185 190
 Ile Lye Asn Ile Leu His Ile Leu Ile Arg Ser Phe Phe Leu Ala Val
 195 200 205
 Arg Ser Asn Ser Glu Lys Arg Lys Glu Phe Cys Asn Val Val Ile Glu
 210 215 220
 Pro Pro Leu Glu Glu Phe Ser Pro Leu Asp Val Asn Lys Ala Asp Glu
 225 230 235 240
 Ile Phe Cys Gly Asp Met Arg Ala Leu
 245

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 339 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Pro Ala Asn Asp Ser Pro Thr Ile Asp Phe Asn Pro Arg Gly Ile
 1 5 10 15
 Leu Arg Asn Ala His Ala Gln Val Ile Leu Ala Thr Ser Gly Leu Arg
 20 25 30
 Lys Ala Phe Leu Lys Arg Thr His Lys Ser Tyr Leu Ser Thr Ala Gln
 35 40 45
 Trp Leu Glu Leu Asp Ala Gly Asn Gly Val Thr Leu Ala Gly Glu Leu
 50 55 60
 Asn Thr Ala Pro Ala Thr Ala Ser Ser Ser His Pro Ala His Lys Asn
 65 70 75 80
 Thr Leu Val Ile Val Leu His Gly Trp Glu Gly Ser Ser Gln Ser Ala
 85 90 95
 Tyr Ala Thr Ser Ala Gly Ser Thr Leu Phe Asp Asn Gly Phe Asp Thr
 100 105 110
 Phe Arg Leu Asn Phe Arg Asp His Gly Asp Thr Tyr His Leu Asn Arg
 115 120 125
 Gly Ile Phe Asn Ser Ser Leu Ile Asp Glu Val Val Gly Ala Val Lys
 130 135 140
 Ala Ile Gln Gln Gln Thr Asp Tyr Asp Lys Tyr Cys Leu Met Gly Phe
 145 150 155 160
 Ser Leu Gly Gly Asn Phe Ala Leu Arg Val Ala Val Arg Glu Gln His
 165 170 175

Leu Ala Lys Pro Leu Ala Gly Val Leu Ala Val Cys Pro Val Leu Asp
 180 185 190
 Pro Ala His Thr Met Met Ala Leu Asn Arg Gly Ala Phe Phe Tyr Gly
 195 200 205
 Arg Tyr Phe Ala His Lys Trp Lys Arg Ser Leu Thr Ala Lys Leu Ala
 210 215 220 225
 Ala Phe Pro Asp Tyr Lys Tyr Gly Lys Asp Leu Lys Ser Ile His Thr
 230 235 240
 Leu Asp Glu Leu Asn Asn Tyr Phe Ile Pro Arg Tyr Thr Gly Phe Asn
 245 250 255
 Ser Val Ser Glu Tyr Phe Lys Ser Tyr Thr Leu Thr Gly Gln Lys Leu
 260 265 270
 Ala Phe Leu Asn Cys Pro Ser Tyr Ile Leu Ala Ala Gly Asp Asp Pro
 275 280 285
 Ile Ile Pro Ala Ser Asp Phe Gln Lys Ile Ala Lys Pro Ala Asn Leu
 290 295 300 305
 His Ile Thr Val Thr Gln Gln Gly Ser His Cys Ala Tyr Leu Glu Asn
 310 315 320
 Leu His Lys Pro Ser Ala Ala Asp Lys Tyr Ala Val Lys Leu Phe Gly
 325 330 335
 Ala Cys

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 311 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Leu Asp Met Pro Ile Asp Pro Val Tyr Tyr Gln Leu Ala Glu Tyr
 1 5 10 15
 Phe Asp Ser Leu Pro Lys Phe Asp Gln Phe Ser Ser Ala Arg Glu Tyr
 20 25 30
 Arg Glu Ala Ile Asn Arg Ile Tyr Glu Glu Arg Asn Arg Gln Leu Ser
 35 40 45
 Gln His Glu Arg Val Glu Arg Val Glu Asp Arg Thr Ile Lys Gly Arg
 50 55 60
 Asn Gly Asp Ile Arg Val Arg Val Tyr Gln Gln Lys Pro Asp Ser Pro
 65 70 75 80
 Val Leu Val Tyr Tyr His Gly Gly Gly Phe Val Ile Cys Ser Ile Glu
 85 90 95
 Ser His Asp Ala Leu Cys Arg Arg Ile Ala Arg Leu Ser Asn Ser Thr
 100 105 110

Val Val Ser Val Asp Tyr Arg Leu Ala Pro Glu His Lys Phe Pro Ala
 115 120 125
 Ala Val Tyr Asp Cys Tyr Aso Ala Thr Lys Trp Val Ala Glu Asn Ala
 130 135 140
 Glu Glu Leu Arg Ile Asp Pro Ser Lys Ile Phe Val Gly Gly Asp Ser
 145 150 155 160
 Ala Gly Gly Asn Leu Ala Ala Ala Val Ser Ile Met Ala Arg Asp Ser
 165 170 175
 Gly Glu Asp Phe Ile Lys His Gln Ile Leu Ile Tyr Pro Val Val Asn
 180 185 190
 Phe Val Ala Pro Thr Pro Ser Leu Leu Glu Phe GLy Glu Gly Leu Trp
 195 200 205
 Ile Leu Asp Gln Lys Ile Met Ser Trp Phe Ser Glu Gln Tyr Phe Ser
 210 215 230
 Arg Glu Glu Aso Lys Phe Asn Pro Leu Ala Ser Val Ile Phe Ala Asp
 235 240 245 250
 Leu Glu Asn Leu Pro Pro Ala Leu Ile Ile Thr Ala Glu Tyr Asp Pro
 255 260 265
 Leu Arg Asp Glu Gly Glu Val Phe Gly Gln Met Leu Arg Arg Ala Gly
 270 275 280
 Val Glu Ala Ser Ile Val Arg Tyr Arg Gly Val Leu His Gly Phe Ile
 285 290 295
 Asn Tyr Tyr Pro Val Leu Lys Ala Ala Arg Asp Ala Ile Asn Gln Ile
 300 305 310
 Ala Ala Leu leu Val Phe Asp
 315 320

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 305 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Pro Leu Asp Pro Arg Ile Lys Lys Leu Leu Glu Ser Ala Leu Thr
 5 10 15
 Ile Pro Ile Gly Lys Ala Pro Val Glu Glu Val Arg Lys Ile Phe Arg
 20 25 30
 Gln Leu Ala Ser Ala Ala Pro Lys Val Glu Val Gly Lys Val Glu Asp
 35 40 45
 Ile Lys Ile Pro Gly Ser Glu Thr Val Ile Asn Ala Arg Val Tyr Phe
 50 55 60

Pro Lys Ser Ser Gly Pro Tyr Gly Val Leu Val Tyr Leu His Gly Gly
 65 70 75 80
 Gly Phe Val Ile Gly Asp Val Glu Ser Tyr Asp Pro Leu Cys Arg Ala
 85 90 95
 Ile Thr Asn Ala Cys Asn Cys Val Val Val Ser Val Asp Tyr Arg Leu
 100 105 110
 Ala Pro Glu Tyr Lys Phe Pro Ser Ala Val Ile Asp Ser Phe Asp Ala
 115 120 125
 Thr Asn Trp Val Tyr Asn Asn Leu Asp Lys Phe Asp Gly Lys Met Gly
 130 135 140
 Val Ala Ile Ala Gly Asp Ser Ale Gly Gly Asn Leu Ala Ala Val Val
 145 150 155 160
 Ala Leu Leu Ser Lys Gly Lys Ile Asn Leu Lys Tyr Gln Ile Leu Val
 165 170 175
 Tyr Pro Ala Val Ser Leu Asp Asn Val Ser Arg Ser Met Ile Glu Tyr
 180 185 190
 Ser Asp Gly Phe Phe Leu Thr Arg Glu His Ile Glu Trp Phe Gly Ser
 195 200 205
 Gln Tyr Leu Arg Ser Pro Ala Asp Leu Leu Asp Phe Arg Phe Ser Pro
 210 215 220
 Ile Leu Ala Gln Asp Phe Asn Gly Leu Pro Pro Ala Leu Ile Ile Thr
 225 230 235 240
 Ala Glu Tyr Asp Pro Leu Arg Asp Gln Gly Glu Ala Tyr Ala Asn Lys
 245 250 255
 Leu Leu Gln Ala Gly Val Ser Val Thr Ser Val Arg Phe Asn Asn Val
 260 265 270
 Ile His Gly Phe Leu Ser Phe Phe Pro Leu Met Glu Gln Gly Arg Asp
 275 280 285
 Ala Ile Gly Leu Ile Gly Ser Val Leu Arg Arg Val Phe Tyr Asp Lys
 290 295 300
 Ile
 305